



#5

SEQUENCE LISTING

<110> Andersen, Carsten
Borchert, Torben Vedel
Nielsen, Bjarne Ronfeldt

<120> Amylase Variants

<130> 10004.204-US

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<170> PatentIn version 3.1

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<211> 1455

<212> DNA

<213> Bacillus sp.

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<221> CDS

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<223> SP690

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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala	
20 25 30	

aac tta aag agt aaa ggg ata aca gct gta tgg atc cca cct gca tgg	144
Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp	
35 40 45	

aag ggg act tcc cag aat gat gta ggt tat gga gcc tat gat tta tat	192
Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr	
50 55 60	

gat ctt gga gag ttt aac cag aag ggg acg gtt cgt aca aaa tat gga	240
Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly	
65 70 75 80	

aca cgc aac cag cta cag gct gcg gtg acc tct tta aaa aat aac ggc	288
Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly	
85 90 95	

att cag gta tat ggt gat gtc gtc atg aat cat aaa ggt gga gca gat	336
Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp	
100 105 110	

ggt acg gaa att gta aat gcg gta gaa gtg aat cgg agc aac cga aac	384
Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn	
115 120 125	

cag gaa acc tca gga gag tat gca ata gaa gcg tgg aca aag ttt gat Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp 130 135 140	432
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ata aaa tat agc ttt acg aga gat tgg ctt aca cat gtg cgt aac acc Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr 245 250 255	768
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cat cca aca cat gcc gtt act ttt gtt gat aac cat gat tct cag ccc His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro 325 330 335	1008
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tat gca ttg gtt ctg aca agg gaa caa ggt tat cct tcc gta ttt tat	1104
Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr	
355 360 365	
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Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser	
370 375 380	
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Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr	
385 390 395 400	
cag cat gat tac ttt gat cat cat gat att atc ggt tgg aca aga gag	1248
Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu	
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gga aat agc tcc cat cca aat tca ggc ctt gcc acc att atg tca gat	1296
Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp	
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ggt cca ggt ggt aac aaa tgg atg tat gtg ggg aaa aat aaa gcg gga	1344
Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly	
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Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile	
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Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp	
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Phe Pro Gly Arg Gly	Asn Asn His Ser Ser Phe	Lys Trp Arg Trp Tyr		
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His Phe Asp Gly Thr	Asp Trp Asp Gln Ser Arg	Gln Leu Gln Asn Lys		
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Ile Tyr Lys Phe Arg	Gly Thr Gly Lys Ala Trp	Asp Trp Glu Val Asp		
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Thr Glu Asn Gly Asn	Tyr Asp Tyr Leu Met Tyr	Ala Asp Val Asp Met		
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Asp His Pro Glu Val	Ile His Glu Leu Arg Asn	Trp Gly Val Trp Tyr		
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Thr Asn Thr Leu Asn	Leu Asp Gly Phe Arg Ile	Asp Ala Val Lys His		
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Ile Lys Tyr Ser Phe	Thr Arg Asp Trp Leu Thr	His Val Arg Asn Thr		
	245	250	255	
Thr Gly Lys Pro Met	Phe Ala Val Ala Glu Phe	Trp Lys Asn Asp Leu		
	260	265	270	
Gly Ala Ile Glu Asn	Tyr Leu Asn Lys Thr Ser	Trp Asn His Ser Val		
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Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
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 305 310 315 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
 325 330 335

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 340 345 350

Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
 370 375 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
 385 390 395 400

Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
 405 410 415

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
 435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
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Val Trp Val Lys Gln
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<223> SP722

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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser	
20 25 30	
aat cta aga aat aga ggt ata acc gct att tgg att ccg cct gcc tgg	144
Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp	
35 40 45	
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Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr	
50 55 60	
gat tta ggg gaa ttt aat caa aag ggg acg gtt cgt act aag tat ggg	240
Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly	
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Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly	
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gtt caa gtt tat ggg gat gta gtg atg aac cat aaa gga gga gct gat	336
Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp	
100 105 110	
gct aca gaa aac gtt ctt gct gtc gag gtg aat cca aat aac cgg aat	384
Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn	
115 120 125	
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Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr	
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His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg	
165 170 175	
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tat gcg ctt att tta aca aga gaa caa ggc tat ccc tct gtc ttc tat Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr 355 360 365	1104
ggt gac tac tat gga att cca aca cat agt gtc cca gca atg aaa gcc Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala 370 375 380	1152
aag att gat cca atc tta gag gcg cgt caa aat ttt gca tat gga aca Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr 385 390 395 400	1200
caa cat gat tat ttt gac cat cat aat ata atc gga tgg aca cgt gaa Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu 405 410 415	1248
gga aat acc acg cat ccc aat tca gga ctt gcg act atc atg tcg gat	1296

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Gly	Pro	Gly	Gly	Glu	Lys	Trp	Met	Tyr	Val	Gly	Gln	Asn	Lys	Ala	Gly		
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caa	gtt	tgg	cat	gac	ata	act	gga	aat	aaa	cca	gga	aca	gtt	acg	atc	1392	
Gln	Val	Trp	His	Asp	Ile	Thr	Gly	Asn	Lys	Pro	Gly	Thr	Val	Thr	Ile		
		450				455					460						
aat	gca	gat	gga	tgg	gct	aat	ttt	tca	gta	aat	gga	gga	tct	gtt	tcc	1440	
Asn	Ala	Asp	Gly	Trp	Ala	Asn	Phe	Ser	Val	Asn	Gly	Gly	Ser	Val	Ser		
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Ile	Trp	Val	Lys	Arg													
			485														

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Asn	Leu	Arg	Asn	Arg	Gly	Ile	Thr	Ala	Ile	Trp	Ile	Pro	Pro	Ala	Trp		
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Thr	Arg	Ser	Gln	Leu	Glu	Ser	Ala	Ile	His	Ala	Leu	Lys	Asn	Asn	Gly		
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Val	Gln	Val	Tyr	Gly	Asp	Val	Val	Met	Asn	His	Lys	Gly	Gly	Ala	Asp		
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Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
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Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
 145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
 165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
 180 185 190

Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
 195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
 210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
 225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
 245 250 255

Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
 260 265 270

Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
 275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
 290 295 300

Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys
 305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
 325 330 335

Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala
 340 345 350

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
 370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
 385 390 395 400

Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
 405 410 415

Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 420 425 430

Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
 435 440 445

Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
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Ile Trp Val Lys Arg
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 Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
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Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp	
50 55 60	
ctc ggc gaa ttc aat caa aaa ggg acc gtc cgc aca aaa tac gga aca	240
Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr	
65 70 75 80	
aaa gct caa tat ctt caa gcc att caa gcc gcc cac gcc gct gga atg	288
Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met	
85 90 95	
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Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly	
100 105 110	
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Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln	
115 120 125	
gaa atc tcg ggc acc tat caa atc caa gca tgg acg aaa ttt gat ttt	432
Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe	
130 135 140	
ccc ggg cgg ggc aac acc tac tcc agc ttt aag tgg cgc tgg tac cat	480
Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His	
145 150 155 160	
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Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr	
165 170 175	
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Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu	
180 185 190	
aac gga aac tat gac tac tta atg tat gcc gac ctt gat atg gat cat	624
Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His	
195 200 205	
ccc gaa gtc gtg acc gag ctg aaa aac tgg ggg aaa tgg tat gtc aac	672
Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn	
210 215 220	
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Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys	
225 230 235 240	
ttc agt ttt ttt cct gat tgg ttg tcg tat gtg cgt tct cag act ggc	768
Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly	
245 250 255	
aag ccg cta ttt acc gtc ggg gaa tat tgg agc tat gac atc aac aag	816

Lys	Pro	Leu	Phe	Thr	Val	Gly	Glu	Tyr	Trp	Ser	Tyr	Asp	Ile	Asn	Lys		
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ttg	cac	aat	tac	att	acg	aaa	aca	gac	gga	acg	atg	tct	ttg	ttt	gat		864
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tat	tat	ggc	att	cca	caa	tat	aac	att	cct	tcg	ctg	aaa	agc	aaa	atc		1152
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Asp	Pro	Leu	Leu	Ile	Ala	Arg	Arg	Asp	Tyr	Ala	Tyr	Gly	Thr	Gln	His		
385				390						395					400		
gat	tat	ctt	gat	cac	tcc	gac	atc	atc	ggg	tgg	aca	agg	gaa	ggg	ggc		1248
Asp	Tyr	Leu	Asp	His	Ser	Asp	Ile	Ile	Gly	Trp	Thr	Arg	Glu	Gly	Gly		
				405					410					415			
act	gaa	aaa	cca	gga	tcc	gga	ctg	gcc	gca	ctg	atc	acc	gat	ggg	ccg		1296
Thr	Glu	Lys	Pro	Gly	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro		
		420					425						430				
gga	gga	agc	aaa	tgg	atg	tac	gtt	ggc	aaa	caa	cac	gct	gga	aaa	gtg		1344
Gly	Gly	Ser	Lys	Trp	Met	Tyr	Val	Gly	Lys	Gln	His	Ala	Gly	Lys	Val		
		435				440						445					
ttc	tat	gac	ctt	acc	ggc	aac	cgg	agt	gac	acc	gtc	acc	atc	aac	agt		1392
Phe	Tyr	Asp	Leu	Thr	Gly	Asn	Arg	Ser	Asp	Thr	Val	Thr	Ile	Asn	Ser		
	450					455					460						
gat	gga	tgg	ggg	gaa	ttc	aaa	gtc	aat	ggc	ggg	tcg	gtt	tcg	gtt	tgg		1440
Asp	Gly	Trp	Gly	Glu	Phe	Lys	Val	Asn	Gly	Gly	Ser	Val	Ser	Val	Trp		
465				470					475						480		
gtt	cct	aga	aaa	acg	acc	gtt	tct	acc	atc	gct	cgg	ccg	atc	aca	acc		1488
Val	Pro	Arg	Lys	Thr	Thr	Val	Ser	Thr	Ile	Ala	Arg	Pro	Ile	Thr	Thr		

	485		490		495	
cga ccg tgg act ggt gaa ttc gtc cgt tgg acc gaa cca cgg ttg gtg						1536
Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val						
	500		505		510	
gca tgg cct tga						1548
Ala Trp Pro						
	515					
<210> 6						
<211> 515						
<212> PRT						
<213> Bacillus stearothermophilus						
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Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu						
1	5		10		15	
Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn						
	20		25		30	
Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys						
	35		40		45	
Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp						
	50		55		60	
Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr						
65		70		75		80
Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met						
	85		90			95
Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly						
	100		105		110	
Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln						
	115		120		125	
Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe						
	130		135		140	
Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His						
145		150		155		160

Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
165 170 175

Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
180 185 190

Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His
195 200 205

Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn
210 215 220

Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys
225 230 235 240

Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly
245 250 255

Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys
260 265 270

Leu His Asn Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu Phe Asp
275 280 285

Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala
290 295 300

Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
305 310 315 320

Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
325 330 335

Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
340 345 350

Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
355 360 365

Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
370 375 380

Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
385 390 395 400

Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Gly
405 410 415

Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
435 440 445

Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
450 455 460

Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
465 470 475 480

Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr
485 490 495

Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
500 505 510

Ala Trp Pro
515

<210> 7
<211> 1920
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (421)..(1872)
<223> Termamyl

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gagacggaaa aatcgtctta atgcacgata tttatgcaac gttcgcagat gctgctgaag 120
agattattaa aaagctgaaa gcaaaaggct atcaattggg aactgtatct cagcttgaag 180
aagtgaagaa gcagagaggc tattgaataa atgagtagaa gcgccatata gccgcttttc 240
ttttggaaga aaatataggg aaaatggtac ttgttaaaaa ttcggaatat ttatacaaca 300

tcatatgttt cacattgaaa ggggaggaga atcatgaaac aacaaaaacg gctttacgcc	360
cgattgctga cgctgttatt tgcgtcattc ttcttgcctgc ctcatctctgc agcagcggcg	420
gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro 1 5 10 15	468
aat gac ggc caa cat tgg agg cgt ttg caa aac gac tcg gca tat ttg Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu 20 25 30	516
gct gaa cac ggt att act gcc gtc tgg att ccc ccg gca tat aag gga Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly 35 40 45	564
acg agc caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu 50 55 60	612
ggg gag ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys 65 70 75 80	660
gga gag ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn 85 90 95	708
gtt tac ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr 100 105 110	756
gaa gat gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val 115 120 125	804
att tca gga gaa cac cta att aaa gcc tgg aca cat ttt cat ttt ccg Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro 130 135 140	852
ggg cgc ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe 145 150 155 160	900
gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys 165 170 175	948
ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn 180 185 190	996
tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val 195 200 205	1044

gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln 210 215 220	1092
ttg gac ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe 225 230 235 240	1140
ttg cgg gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met 245 250 255	1188
ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn 260 265 270	1236
tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu 275 280 285	1284
cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met 290 295 300	1332
agg aaa ttg ctg aac ggt acg gtc gtt tcc aag cat ccg ttg aaa tcg Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser 305 310 315 320	1380
gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu 325 330 335	1428
tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu 340 345 350	1476
aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly 355 360 365	1524
acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile 370 375 380	1572
gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His 385 390 395 400	1620
gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp 405 410 415	1668
agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro 420 425 430	1716
ggc ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca	1764

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
 435 440 445
 tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg 1812
 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460
 gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat 1860
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480
 gtt caa aga tag aagagcagag aggacggatt tcctgaagga aatccgtttt 1912
 Val Gln Arg
 tttatttt 1920
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 <211> 483
 <212> PRT
 <213> Bacillus licheniformis
 <400> 8
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 Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
 20 25 30
 Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45
 Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
 50 55 60
 Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80
 Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
 85 90 95
 Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
 100 105 110
 Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
 115 120 125

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
 130 135 140

Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
 145 150 155 160

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
 165 170 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
 180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
 195 200 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
 210 215 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
 225 230 235 240

Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
 245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
 260 265 270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
 275 280 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
 290 295 300

Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
 305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly

355 360 365
 Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
 370 375 380
 Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
 385 390 395 400
 Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
 405 410 415
 Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430
 Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
 435 440 445
 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480
 Val Gln Arg

<210> 9
 <211> 2084
 <212> DNA
 <213> Bacillus amyloliquefaciens

<220>
 <221> CDS
 <222> (343)..(1794)
 <223> BAN

<400> 9
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 ctgaagaagt ggatcgattg tttgagaaaa gaagaagacc ataaaaatac cttgtctgtc 120
 atcagacagg gtatttttta tgctgtccag actgtccgct gtgtaaaaat aaggaataaa 180
 ggggggttgt tattatttta ctgatatgta aaatataatt tgtataagaa aatgagaggg 240
 agaggaaaca tgattcaaaa acgaaagcgg acagtttcgt tcagacttgt gcttatgtgc 300

acgctgttat ttgtcagttt gccgattaca aaaacatcag cc gta aat ggc acg	354
Val Asn Gly Thr	
1	
ctg atg cag tat ttt gaa tgg tat acg ccg aac gac ggc cag cat tgg	402
Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp Gly Gln His Trp	
5 10 15 20	
aaa cga ttg cag aat gat gcg gaa cat tta tcg gat atc gga atc act	450
Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp Ile Gly Ile Thr	
25 30 35	
gcc gtc tgg att cct ccc gca tac aaa gga ttg agc caa tcc gat aac	498
Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser Gln Ser Asp Asn	
40 45 50	
gga tac gga cct tat gat ttg tat gat tta gga gaa ttc cag caa aaa	546
Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Gln Gln Lys	
55 60 65	
ggg acg gtc aga acg aaa tac ggc aca aaa tca gag ctt caa gat gcg	594
Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu Leu Gln Asp Ala	
70 75 80	
atc ggc tca ctg cat tcc cgg aac gtc caa gta tac gga gat gtg gtt	642
Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr Gly Asp Val Val	
85 90 95 100	
ttg aat cat aag gct ggt gct gat gca aca gaa gat gta act gcc gtc	690
Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp Val Thr Ala Val	
105 110 115	
gaa gtc aat ccg gcc aat aga aat cag gaa act tcg gag gaa tat caa	738
Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser Glu Glu Tyr Gln	
120 125 130	
atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt gga aac acg tac	786
Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg Gly Asn Thr Tyr	
135 140 145	
agt gat ttt aaa tgg cat tgg tat cat ttc gac gga gcg gac tgg gat	834
Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Ala Asp Trp Asp	
150 155 160	
gaa tcc ccg aag atc agc cgc atc ttt aag ttt cgt ggg gaa gga aaa	882
Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg Gly Glu Gly Lys	
165 170 175 180	
gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac tat gac tat tta	930
Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn Tyr Asp Tyr Leu	
185 190 195	
atg tat gct gat gtt gac tac gac cac cct gat gtc gtg gca gag aca	978
Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val Val Ala Glu Thr	
200 205 210	
aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca tta gac ggc ttc	1026

Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	Leu	Ser	Leu	Asp	Gly	Phe	
		215					220					225				
cgt	att	gat	gcc	gcc	aaa	cat	att	aaa	ttt	tca	ttt	ctg	cgt	gat	tgg	1074
Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg	Asp	Trp	
	230					235					240					
ggt	cag	gcg	gtc	aga	cag	gcg	acg	gga	aaa	gaa	atg	ttt	acg	ggt	gcg	1122
Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	Glu	Met	Phe	Thr	Val	Ala	
245					250					255					260	
gag	tat	tgg	cag	aat	aat	gcc	ggg	aaa	ctc	gaa	aac	tac	ttg	aat	aaa	1170
Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	Glu	Asn	Tyr	Leu	Asn	Lys	
				265					270					275		
aca	agc	ttt	aat	caa	tcc	gtg	ttt	gat	ggt	ccg	ctt	cat	ttc	aat	tta	1218
Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Phe	Asn	Leu	
			280					285					290			
cag	gcg	gct	tcc	tca	caa	gga	ggc	gga	tat	gat	atg	agg	cgt	ttg	ctg	1266
Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Arg	Leu	Leu	
		295				300						305				
gac	ggt	acc	ggt	gtg	tcc	agg	cat	ccg	gaa	aag	gcg	ggt	aca	ttt	ggt	1314
Asp	Gly	Thr	Val	Val	Ser	Arg	His	Pro	Glu	Lys	Ala	Val	Thr	Phe	Val	
	310					315					320					
gaa	aat	cat	gac	aca	cag	ccg	gga	cag	tca	ttg	gaa	tcg	aca	gtc	caa	1362
Glu	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr	Val	Gln	
325					330					335					340	
act	tgg	ttt	aaa	ccg	ctt	gca	tac	gcc	ttt	att	ttg	aca	aga	gaa	tcc	1410
Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg	Glu	Ser	
				345					350					355		
ggt	tat	cct	cag	gtg	ttc	tat	ggg	gat	atg	tac	ggg	aca	aaa	ggg	aca	1458
Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys	Gly	Thr	
		360					365					370				
tcg	cca	aag	gaa	att	ccc	tca	ctg	aaa	gat	aat	ata	gag	ccg	att	tta	1506
Ser	Pro	Lys	Glu	Ile	Pro	Ser	Leu	Lys	Asp	Asn	Ile	Glu	Pro	Ile	Leu	
		375					380					385				
aaa	gcg	cgt	aag	gag	tac	gca	tac	ggg	ccc	cag	cac	gat	tat	att	gac	1554
Lys	Ala	Arg	Lys	Glu	Tyr	Ala	Tyr	Gly	Pro	Gln	His	Asp	Tyr	Ile	Asp	
	390					395				400						
cac	ccg	gat	gtg	atc	gga	tgg	acg	agg	gaa	ggt	gac	agc	tcc	gcc	gcc	1602
His	Pro	Asp	Val	Ile	Gly	Trp	Thr	Arg	Glu	Gly	Asp	Ser	Ser	Ala	Ala	
405					410					415					420	
aaa	tca	ggt	ttg	gcc	gct	tta	atc	acg	gac	gga	ccc	ggc	gga	tca	aag	1650
Lys	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	Gly	Gly	Ser	Lys	
				425					430					435		
cgg	atg	tat	gcc	ggc	ctg	aaa	aat	gcc	ggc	gag	aca	tgg	tat	gac	ata	1698
Arg	Met	Tyr	Ala	Gly	Leu	Lys	Asn	Ala	Gly	Glu	Thr	Trp	Tyr	Asp	Ile	

440	445	450	
acg ggc aac cgt tca gat act gta aaa atc gga tct gac ggc tgg gga			1746
Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser Asp Gly Trp Gly			
455	460	465	
gag ttt cat gta aac gat ggg tcc gtc tcc att tat gtt cag aaa taa			1794
Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr Val Gln Lys			
470	475	480	
ggtaataaaaa aaacacctcc aagctgagtg cgggtatcag cttggaggtg cgtttatattt			1854
ttcagccgta tgacaaggtc ggcatcaggt gtgacaaata cggtatgctg gctgtcatag			1914
gtgacaaatc cgggtttttgc gccgttttggc tttttcacat gtctgatttt tgtataatca			1974
acaggcacgg agccggaatc ttctgccttg gaaaaataag cggcgatcgt agctgcttcc			2034
aatatggatt gttcatcggg atcgtctgctt ttaatcaciaa cgtgggatcc			2084

<210> 10
 <211> 483
 <212> PRT
 <213> Bacillus amyloliquefaciens

<400> 10

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
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Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
20 25 30

Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
35 40 45

Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
50 55 60

Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65 70 75 80

Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
85 90 95

Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
100 105 110

Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser

115	120	125
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg 130 135 140		
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly 145 150 155 160		
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg 165 170 175		
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn 180 185 190		
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val 195 200 205		
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser 210 215 220		
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe 225 230 235 240		
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met 245 250 255		
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn 260 265 270		
Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu 275 280 285		
His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met 290 295 300		
Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala 305 310 315 320		
Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu 325 330 335		
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu 340 345 350		

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
 370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
 385 390 395 400

Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
 405 410 415

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430

Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
 435 440 445

Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
 450 455 460

Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
 465 470 475 480

Val Gln Lys

<210> 11
 <211> 1458
 <212> DNA
 <213> Bacillus sp.

<220>
 <221> CDS
 <222> (1)..(1458)
 <223> AA560

<400> 11
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 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
 1 5 10 15

cta cca aat gac gga aac cat tgg aat aga tta agg tct gat gca agt 96
 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
 20 25 30

aac cta aaa gat aaa ggg atc tca gcg gtt tgg att cct cct gca tgg	144
Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp	
35 40 45	
aag ggt gcc tct caa aat gat gtg ggg tat ggt gct tat gat ctg tat	192
Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr	
50 55 60	
gat tta gga gaa ttc aat caa aaa gga acc att cgt aca aaa tat gga	240
Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly	
65 70 75 80	
acg cgc aat cag tta caa gct gca gtt aac gcc ttg aaa agt aat gga	288
Thr Arg Asn Gln Leu Gln Ala Ala Val Asn Ala Leu Lys Ser Asn Gly	
85 90 95	
att caa gtg tat ggc gat gtt gta atg aat cat aaa ggg gga gca gac	336
Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp	
100 105 110	
gct acc gaa atg gtt agg gca gtt gaa gta aac ccg aat aat aga aat	384
Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn	
115 120 125	
caa gaa gtg tcc ggt gaa tat aca att gag gct tgg aca aag ttt gac	432
Gln Glu Val Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp	
130 135 140	
ttt cca gga cga ggt aat act cat tca aac ttc aaa tgg aga tgg tat	480
Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr	
145 150 155 160	
cac ttt gat gga gta gat tgg gat cag tca cgt aag ctg aac aat cga	528
His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Lys Leu Asn Asn Arg	
165 170 175	
att tat aaa ttt aga ggt gat gga aaa ggg tgg gat tgg gaa gtc gat	576
Ile Tyr Lys Phe Arg Gly Asp Gly Lys Gly Trp Asp Trp Glu Val Asp	
180 185 190	
aca gaa aac ggt aac tat gat tac cta atg tat gca gat att gac atg	624
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met	
195 200 205	
gat cac cca gag gta gtg aat gag cta aga aat tgg ggt gtt tgg tat	672
Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr	
210 215 220	
acg aat aca tta ggc ctt gat ggt ttt aga ata gat gca gta aaa cat	720
Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His	
225 230 235 240	
ata aaa tac agc ttt act cgt gat tgg att aat cat gtt aga agt gca	768
Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala	
245 250 255	

act ggc aaa aat atg ttt gcg gtt gcg gaa ttt tgg aaa aat gat tta	816
Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu	
260 265 270	
ggt gct att gaa aac tat tta aac aaa aca aac tgg aac cat tca gtc	864
Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val	
275 280 285	
ttt gat gtt ccg ctg cac tat aac ctc tat aat gct tca aaa agc gga	912
Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly	
290 295 300	
ggg aat tat gat atg agg caa ata ttt aat ggt aca gtc gtg caa aga	960
Gly Asn Tyr Asp Met Arg Gln Ile Phe Asn Gly Thr Val Val Gln Arg	
305 310 315 320	
cat cca atg cat gct gtt aca ttt gtt gat aat cat gat tcg caa cct	1008
His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro	
325 330 335	
gaa gaa gct tta gag tct ttt gtt gaa gaa tgg ttc aaa cca tta gcg	1056
Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala	
340 345 350	
tat gct ttg aca tta aca cgt gaa caa ggc tac cct tct gta ttt tat	1104
Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr	
355 360 365	
gga gat tat tat ggc att cca acg cat ggt gta cca gcg atg aaa tcg	1152
Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser	
370 375 380	
aaa att gac ccg att cta gaa gcg cgt caa aag tat gca tat gga aga	1200
Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Arg	
385 390 395 400	
caa aat gac tac tta gac cat cat aat atc atc ggt tgg aca cgt gaa	1248
Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu	
405 410 415	
ggg aat aca gca cac ccc aac tcc ggt tta gct act atc atg tcc gat	1296
Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp	
420 425 430	
ggg gca gga gga aat aag tgg atg ttt gtt ggg cgt aat aaa gct ggt	1344
Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly	
435 440 445	
caa gtt tgg acc gat atc act gga aat cgt gca ggt act gtt acg att	1392
Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile	
450 455 460	
aat gct gat gga tgg ggt aat ttt tct gta aat gga gga tca gtt tct	1440
Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser	
465 470 475 480	
att tgg gta aac aaa taa	1458

Ile Trp Val Asn Lys
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<210> 12
<211> 485
<212> PRT
<213> Bacillus sp.

<400> 12

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
20 25 30

Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Asn Gln Leu Gln Ala Ala Val Asn Ala Leu Lys Ser Asn Gly
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Val Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Lys Leu Asn Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Gly Trp Asp Trp Glu Val Asp
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala
245 250 255

Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly
290 295 300

Gly Asn Tyr Asp Met Arg Gln Ile Phe Asn Gly Thr Val Val Gln Arg
305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Arg
385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
435 440 445

Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Asn Lys
485

<210> 13
<211> 485
<212> PRT
<213> bacillus sp. 707

<400> 13

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Asn Ser Asp Ala Ser
20 25 30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Ser Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn

115		120		125
Gln Glu Val Thr Gly Glu Tyr Thr Ile Glu Ala Trp Thr Arg Phe Asp				
130		135		140
Phe Pro Gly Arg Gly Asn Thr His Ser Ser Phe Lys Trp Arg Trp Tyr				
145		150		155
				160
His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Arg Leu Asn Asn Arg				
		165		170
				175
Ile Tyr Lys Phe Arg Gly His Gly Lys Ala Trp Asp Trp Glu Val Asp				
		180		185
				190
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met				
		195		200
				205
Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr				
		210		215
				220
Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His				
		225		230
				235
				240
Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala				
		245		250
				255
Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu				
		260		265
				270
Gly Ala Ile Glu Asn Tyr Leu Gln Lys Thr Asn Trp Asn His Ser Val				
		275		280
				285
Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly				
		290		295
				300
Gly Asn Tyr Asp Met Arg Asn Ile Phe Asn Gly Thr Val Val Gln Arg				
		305		310
				315
				320
His Pro Ser His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro				
		325		330
				335
Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala				
		340		345
				350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Arg Ser
 370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Lys
 385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
 405 410 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 420 425 430

Gly Ala Gly Gly Ser Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
 435 440 445

Gln Val Trp Ser Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
 450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
 465 470 475 480

Ile Trp Val Asn Lys
 485

<210> 14
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 14
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<210> 15
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 15	
gaatttgtag atacgatttt g	21
<210> 16	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 16	
cgattgctga cgctgttatt tgcg	24
<210> 17	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 17	
cttgttccct tgtcagaacc aatg	24
<210> 18	
<211> 30	
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<213> Artificial Sequence	
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gtcatagttg ccgaaatctg tatcgacttc	30
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<211> 20	
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gacctgcagt caggcaacta	20
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<223> Primer

<400> 20

tagagtcgac ctgcagggcat

20